

GROWTH ARREST HOMEBOX GENE

BACKGROUND OF THE INVENTION

The leading cause of death in the United States and in most developed countries, is atherosclerosis. Atherosclerosis is a disease affecting the large and medium size muscular arteries such as the coronary or carotid arteries and the large elastic arteries such as the aorta, iliac, and femoral arteries. This disease causes narrowing and calcification of arteries. The narrowing results from deposits of substances in the blood in combination with proliferating vascular smooth muscle cells.

The deposits known as atherosclerotic plaques are comprised of lipoproteins, mainly cholesterol, proliferating vascular smooth muscle cells and fibrous tissue, and extracellular matrix components, which are secreted by vascular smooth muscle cells. As the plaques grow, they narrow the lumen of the vessel decreasing arterial blood flow and weakening the effected arteries. The resulting complications potentially include a complete blockage of the lumen of the artery, with ischemia and necrosis of the organ supplied by the artery, ulceration and thrombus formation with associated embolism, calcification, and aneurysmal dilation. When atherosclerosis causes occlusion of the coronary arteries, it leads to myocardial dysfunction, ischemia and infarction and often death. Indeed, 20-25% of deaths in the United States are attributable to atherosclerotic heart disease. Atherosclerosis also leads to lower extremity gangrene, strokes, mesenteric occlusion, ischemic encephalopathy, and renal failure, depending on the specific vasculature involved. Approximately 50% of all deaths in the United States can be attributed to atherosclerosis and its complications.

Present treatments for atherosclerosis include drugs and surgery, including balloon angioplasty. As a result of angioplasty, vascular smooth muscle cells de-differentiate and proliferate and leading to reocclusion of the vessel. These de-differentiated vascular smooth muscle cells deposit collagen and other matrix substances, that contribute to the narrowing of vessel. Vascular cells secrete growth factors such as platelet derived growth factor, which induces both chemotaxis and proliferation of vascular smooth muscle cells.

Many of the present drug therapies treat a predisposing condition such as hyperlipidemia, hypertension, and hypercholesterolemia, in an attempt to slow or halt the progression of the disease. Other drug therapies are aimed at preventing platelet aggregation or the coagulation cascade. Unfortunately, the drug treatments do not reverse existing conditions.

Surgical treatments include coronary artery bypass grafting, balloon angioplasty, or vessel endarterectomy which, when successful, bypass or unblock occluded arteries thereby restoring blood flow through the artery. The surgical treatments do not halt or reverse the progression of the disease because they do not affect smooth muscle cell proliferation and secretion of extracellular matrix components.

The bypass surgeries, particularly the coronary bypass surgeries, are major, complicated surgeries which involve a significant degree of risk. The balloon angioplasty, while also a surgical procedure, is less risky. In balloon angioplasty, a catheter having a deflated balloon is inserted into an artery and positioned next to the plaque. The balloon is inflated thereby compressing the plaque against the arterial wall. As a result, the occlusion is decreased and increased blood flow is restored. However, the balloon

angioplasty injures the arterial wall. As a result, the underlying vascular smooth muscle cells migrate to the intima, and synthesize and excrete extracellular matrix components eventually leading to the reocclusion of the vessel. Of the estimated 400,000 coronary artery balloon angioplasties performed each year in the United States, 40% fail due to reocclusion requiring a repeat procedure or coronary bypass surgery. Bypass surgeries also have a significant rate of failure due to internal hyperplasia, which involves excessive proliferation of vascular smooth muscle cells at the sites of vascular anastomoses.

Attempts have been made to prevent reocclusion of vessels after balloon angioplasties in experimental animals. One approach has been to treat rat carotid arteries with antisense oligonucleotides directed against the c-myb gene following balloon angioplasty de-endothelialization. In vascular smooth muscle cells expression of the c-myb gene is up-regulated during the G1 to S transition of the cell cycle, and the activation of c-myb expression is required for further cell cycle progression. The antisense oligonucleotides to c-myb blocked smooth muscle cell proliferation following balloon angioplasty. However, the antisense oligonucleotides are applied in a pleuronic gel to the adventitia, that is, the exterior, rather than the lumen side of the affected vessel. Exposing the exterior of the vessel requires additional surgery with its attendant risks, and is therefore not desirable.

It would be desirable to have a nonsurgical treatment, used in conjunction with balloon angioplasties to reduce vascular smooth muscle cell proliferation.

SUMMARY OF THE INVENTION

A novel growth arrest homeobox gene has been discovered and the nucleotide sequences have been determined in both the rat and the human. The expression of the novel homeobox gene inhibits vascular smooth muscle cell growth. The growth arrest homeobox gene hereinafter referred to as the "Gax gene" and its corresponding proteins are useful in the study of vascular smooth muscle cell proliferation and in the treatment of blood vessel diseases that result from excessive smooth muscle cell proliferation, particularly after balloon angioplasty.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is the nucleotide sequence SEQ. ID. NO. 1 of rat Gax gene with the predicted amino acid sequence SEQ. ID. NO. 2 listed below the nucleotide sequence. The homeobox is indicated by a box, and the CAX nucleotide repeat, where X is either cytosine or guanine, is underlined. A polyadenylation signal is in boldface and italics. Putative consensus sites are indicated as follows: for phosphorylation by protein kinase C, circles; for cyclic AMP (cAMP)-dependent protein kinase, squares; for casein kinase II, diamonds; and for histone H1 kinase, triangles. Residues which could potentially be a target for either cAMP-dependent protein kinase or protein kinase C are both circled and boxed.

FIG. 2 is the map of mouse chromosome 12 showing the location of the Gax gene;

FIG. 3 is the nucleotide sequence SEQ. ID. NO. 3 of human Gax gene with the predicted amino acid sequence SEQ. ID. NO. 4 listed below the nucleotide sequence;

FIG. 4 is a map of human Gax gene showing how the separately cloned fragments were joined and oriented in the plasmid, Bluescript IISK+;

FIG. 5A is a northern blot showing Gax RNA levels in vascular smooth muscle cells in response to 10% fetal calf

serum after 4, 24, and 48 hours; lane Q is RNA from quiescent cells; GAPDH is rat glyceraldehyde 3-phosphate dehydrogenase;

FIG. 5B is a northern blot showing Gax RNA levels and Hox 1.3 RNA levels in vascular smooth muscle cells in response to 10 ng/ml human platelet derived growth factor at 0.25, 0.5, 1, 2, and 4 hours, lane Q is RNA from quiescent vascular smooth muscle cells;

FIG. 6 is a graph of changes in relative Gax mRNA levels in vascular smooth muscle cells in response to 10% fetal calf serum and 10 ng/ml of the PDGF isoforms; the circles represent PDGF-AA, the squares represent PDGF-BB, the diamonds represent fetal calf serum, and the triangles represent PDGF-AB;

FIG. 7 is a graph showing ³H-thymidine uptake in vascular smooth muscle cells at various times after stimulation with fetal calf serum and PDGF isoforms; the circles represent PDGF-AA, the triangles represent PDGF-AB, the squares represent PDGF-BB, the diamonds represent fetal calf serum, and the solid squares represent no mitogen;

FIG. 8 is a graph showing relative Gax mRNA levels in vascular smooth muscle cells in response to varying doses of PDGF-AB, represented by triangles, and PDGF-BB, represented by squares;

FIG. 9 is a graph showing relative Gax mRNA levels in vascular smooth muscle cells in response to varying doses of fetal calf serum;

FIG. 10 is a graph showing relative Gax mRNA levels in vascular smooth muscle cells in response to fetal calf serum withdrawal;

FIG. 11 is a dose response curve showing % inhibition of growth in vascular smooth muscle cells in response to varying doses of microinjected GST-Gax protein;

FIG. 12 is a graph showing percent inhibition of mitogen induced DNA synthesis in vascular smooth muscle cells in response to: ras (Leu-61) protein; ras (Leu-61) protein in combination with the GST-Gax protein; GST-Gax protein; and the GST;

FIG. 13 is a graph showing percent inhibition of vascular smooth muscle cell entry into S phase by microinjected GST-Gax protein over time and the ³H-thymidine uptake over the same time period;

FIG. 14 is a graph showing the ratio of the Gax mRNA to glyceraldehyde-3-phosphate dehydrogenase designated "G3" level from normal vascular tissue and times following acute blood vessel injury.

DETAILED DESCRIPTION OF THE INVENTION

A novel gene, the Gax gene, has been discovered, the expression of which inhibits vascular smooth muscle cell growth. The Gax gene and the protein it encodes, referred to herein as the "Gax protein" are useful in the study of vascular smooth muscle cell proliferation and in inhibiting smooth muscle cell proliferation. The inhibition of vascular smooth muscle cell proliferation, particularly by genetic therapy, is also useful in the treatment of vascular diseases associated with excessive smooth muscle cell proliferation.

Nucleotide sequences, such as the Gax gene or portions thereof, or mRNA are administered to the vascular cells, preferably during a balloon angioplasty procedure, to inhibit the proliferation of vascular smooth muscle cells. The nucleotide sequences are delivered, preferably to the interior of the vessel wall during balloon angioplasty procedure preferably by a perforated balloon catheter. Genes are transferred

from vectors into vascular smooth muscle cells in vivo where the genes are expressed. Suitable vectors and procedures for the transfer of nucleotides are found in

Nabel, E. G., et al. "Site-Specific Gene Expression in Vivo by Direct Gene Transfer into the Arterial Wall" (1990) *Science* Vol. 249, pp. 1285-1288, which is incorporated herein by reference. Specialized perforated balloon catheters which deliver nucleotide sequences to vessel walls employing viral and non-viral vectors are used for delivery of nucleotide sequences and a description of the catheter's structure and use may be found in Flugelman M. Y., et al. "Low Level In Vivo Gene Transfer Into the Arterial Wall Through a Perforated Balloon Catheter" *Circulation*, Vol. 85, No. 3, pp. 1110-1117 (March 1992) which is incorporated herein by reference.

Genetic therapy, preferably by the over expression of the Gax gene, restores the proliferating vascular smooth muscle cells to a more normal phenotype, thus preventing or reducing the smooth muscle proliferation that is associated with the formation of the atherosomatous plaque and with internal arterial thickening following balloon angioplasty. In addition to preventing or reducing the reocclusion of the vessel, such genetic therapy decreases the risks associated with additional surgeries. Also, the Gax proteins or portions thereof, are administered to vascular cells preferably employing the perforated catheter, to inhibit the proliferation of vascular smooth muscle cells.

The molecular control of cellular proliferation is not well understood. A class of genes, known as Homeobox genes, encode a class of transcription factors which are important in embryogenesis, tissue specific gene expression and cell differentiation. The homeobox genes share a highly conserved 183 nucleotide sequence that is referred to as the "homeobox". The homeobox encodes a 61 amino acid helix-turn-helix motif that binds to adenine and thymine rich gene regulatory sequences with high affinity. Several vertebrate homeobox proteins have been shown to be transcription factors required for expression of lineage-specific genes. The tissue-specific transcription factors bind to DNA and repress or induce groups of subordinate genes. Many, but not all of these homeobox genes are located in one of four major clusters known as Hox clusters, designated Hox-1, Hox-2, Hox-3 and Hox-4. The Hox genes are expressed in the developing embryo, in distinct overlapping spatial patterns along the anterior-posterior axis which parallels the Hox gene order along the chromosome. Homeobox transcription factors control axial patterning, cell migration and differentiation in the developing embryo and are involved in the maintenance of tissue specific gene expression in adult organisms.

A new homeobox gene has been discovered, isolated and sequenced in both the rat and human. This new gene is a growth arrest specific homeobox gene and is referred to herein as the "Gax gene". The expression of the Gax gene is restricted to the cardiovascular system, and in particular, to vascular smooth muscle cells where it functions as a negative regulator of cell proliferation.

Isolation of the rat Gax cDNA

An adult rat aorta cDNA library in λ ZAP, from Stratagene, was screened with a 64-fold degenerate 29-mer oligonucleotide containing three inosine residues directed at the most highly conserved region of the antennapedia homeodomain (helix 3), with the following sequence SEQ. ID. NO. 5, where I represents inosine:

5'-AA(A/G)AITGGTT(T/C)CA(A/G)AA(C/T)(A/C)GI(A/C)
GIATGAA-3'

Recombinant phage colonies in *Escherichia coli* were adsorbed in duplicate to nitrocellulose membranes and hybridized at 42° C. with this oligonucleotide end labeled with (T-32P)ATP in a mixture containing 0.5M sodium phosphate at pH 7.0, 7% sodium dodecyl sulfate, 1 mM EDTA, and 1% bovine serum albumin. The filters were washed with a final stringency of 0.5×SSC (1×SSC in 150 mM NaCl with 15 mM sodium citrate at pH 7.0)-0.1% sodium dodecyl sulfate at 42° C. and exposed to X-ray film. Thirteen positive signals were isolated and rescreened until the clones were plaque purified. The plasmids containing the clones in λ ZAP vector were then excised by the protocol recommended by the manufacturer and sequenced on both strands with sequenase version 2.0 from United States Biochemicals. From 500,000 plaques, 13 positive clones were isolated, 12 of which contained homeodomains. Nine of the isolated clones were derived from previously described homeobox genes: Hox-1.3, Hox-1.4, Hox-1.11, and rat homeobox R1b. However, three clones represented the cDNA designated herein as the "Gax" gene. Homology searches were performed via the GenBank and EMBL data bases, version 73, by using the BLAST algorithm (4).

Nucleotide Sequence of the rat Gax Gene

The nucleotide sequence of the rat Gax gene SEQ. ID. NO. 1 is shown in FIG. 1. The cDNA encoding Gax is 2,244 base pairs in length, which corresponds to the size of the Gax transcript, that is the Gax mRNA, which is about 2.3 to 2.4 kb as determined by Northern blot analysis. The Gax cDNA has an open reading frame from nucleotide residues 197 to 1108 beginning with an in-frame methionine that conforms to the eukaryotic consensus sequence for the start of translation and is preceded by multiple stop codons in all three reading frames. The open reading frame of the cDNA predicts a 33.6-kDa protein SEQ. ID. NO. 2 containing 303 amino acids with a homeodomain from amino acid residues 185 to 245, as shown in FIG. 1. To confirm that this cDNA was capable of producing a protein product, the Gax open reading frame was fused in frame to the pQE-9 *E. coli* expression vector, from Qiagen, Inc., Chatsworth, Calif. and expressed in bacteria according to Hochuli, E., et. al. (1988) "Genetic Approach to Facilitate Purification of Recombinant Proteins with a Novel Metal Chelate Adsorbent" *Bio/Technology* Vol. 6, pp. 1321-1325. *E. coli* containing this plasmid expressed a new protein of about 30 to about 36 kDa as determined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis, and extracts from these *E. coli* cells displayed a weak binding activity for the adenine and thymine rich, MHOX-binding site in the creatine kinase M enhancer.

The cDNA encoding the rat Gax gene also contains a long 3'-untranslated region, from bases 1109 to 2244, with a polyadenylation signal at base 2237, as shown in FIG. 1. The region between amino acids 87 and 184 contains 23 serine amino acids out of 88 amino acids and 10 proline amino acids out of 88 amino acids and contains several consensus sequences for phosphorylation by protein kinases. Gax also possesses a structural feature which is also found in several transcription factors, including homeodomain proteins, known as the CAX or Opa transcribed repeat. The Opa transcribed repeat encodes a stretch of glutamines and histidines; in the rat Gax gene it encodes 18 residues, of which 12 are consecutive histidines. This motif is shared by other transcription factors, such as the zinc finger gene YY-1, as well as by several homeobox genes, including H2.0, HB24, ERA-1 (Hox-1.6), Dual bar, and Tes-1. The Gax protein may require post-translational modifications for full activity, modifications that bacterially produced proteins

do not undergo. Since the Gax protein has multiple consensus sites for phosphorylation by protein kinases, it is possible that its activity is activated or otherwise modulated by phosphorylation at one or more of those sites.

The Gax Gene Maps to a Chromosome 12 of the Mouse Genome

Gax is located on chromosome 12 as shown in FIG. 2 of the mouse and is not a part of the Hox-1, Hox-2, Hox-3, or Hox-4 gene clusters, which are located on chromosomes 6, 11, 15, and 2, respectively, McGinnis, W., and R. Krumlauf, (1992) "Homeobox genes and Axial Patterning" *Cell*, Vol. 68, pp. 283-302. Also Gax does not cosegregate with any other homeobox genes previously mapped in the interspecific backcross. A comparison was done of the interspecific map of chromosome 12 with a composite mouse linkage map that reports the map location of many uncloned mouse mutations using GBASE, a computerized data base maintained at The Jackson Laboratory, Bar Harbor, Me. The Gax gene mapped in a region of the composite map that lacks mouse mutations with a phenotype that might be expected for an alteration in this locus.

The mouse chromosomal location of the Gax was determined by interspecific backcross analysis using progeny generated by mating (C57BL/6J×*Mus spreitus*)F₁ females and C57BL/6J males. The C57BL/6J and *M. spreitus* DNAs were digested with several enzymes and analyzed by Southern blot hybridization for informative restriction fragment length polymorphisms with a rat cDNA Gax probe. The probe, a 1,155-bp rat cDNA clone, was labeled with (α -³²P)dCTP by using a random prime labeling kit from Amersham and washing was done with a final stringency of 0.2×SSCP (34)-0.1% sodium dodecyl sulfate, 65° C. A major fragment of 4.2 kb was detected in HincII-digested C57BL/6J DNA, and major fragments of 3.6 and 2.7 kb were detected in HincII-digested *M. spreitus* DNA. The 3.6-kb and 2.7-kb *M. spreitus* HincII restriction fragment length polymorphisms were used to monitor the segregation of the Gax locus in backcross mice. Recombination distances were calculated by using the computer program SPRETUS MADNESS. Gene order was determined by minimizing the number of recombination events required to explain the allele distribution patterns.

The mapping results indicated that the mouse Gax gene is located in the proximal region of mouse chromosome 12 linked to neuroblastoma myc-related oncogene 1 (Nmvc-1), the laminin B1 subunit gene (Lamb-1), a DNA segment, chromosome 12, the Nyu 1 gene (D12Nyu1), and the β -spectrin gene (Spnb-1). The ratios of the total number of mice exhibiting recombinant chromosomes to the total number of mice analyzed for each pair of loci and the most likely gene order are as follows: centromere-Nmvc-1-19/193-Lamb-1-9/166-Gax-10/166-D12Nyu1-19/185-Spnb-1. The recombination frequencies, expressed as genetic distances in centimorgans±the standard error, are as follows: Nmvc-1-9.8±2.2-Lamb-1-5.4±1.8-Gax-6.0±1.9-D12Nyu1-10.3±2.2-Spnb-1.

Gax Gene Expression in Rat Tissue

It has been discovered that the Gax transcript is largely confined to the cardiovascular system, including the descending thoracic aorta, where it is expressed at higher levels than in other tissues, and the heart. Gax gene expression was also detected in the adult lung and kidney where it is found in mesangial cells. No Gax gene expression was detected in the brain, liver, skeletal muscle, spleen, stomach, or testes, nor was expression detected in the intestine or pancreas. In contrast, the Gax gene was more widely expressed in the developing embryo, with the transcript

02755220 010601

detectable in the developing cardiovascular system, multiple mesodermal tissues, and some ectodermal tissues.

The 2.3-kb to 2.4-kb Gax RNA transcript was detected in smooth muscle cells cultured from adult rat aorta, consistent with the *in situ* hybridization findings and the fact that Gax was originally isolated from a vascular smooth muscle library. The Gax transcript was also detected in rat vascular smooth muscle cells transformed by simian virus 40. However, no Gax gene expression was detected in either of two cell lines derived from embryonic rat aortic smooth muscle, A7r5 and A10. The Gax transcript was also not detected in NIH 3T3 fibroblasts, or human foreskin fibroblasts. The Gax transcript was not detected in the skeletal muscle cell line C2C12. A relatively high level of Gax gene expression was detected in cultured rat mesangial cells. Mesangial cells share many similarities to vascular smooth muscle cells, both structurally and functionally, and proliferate abnormally in renal diseases such as glomerulonephritis and glomerulosclerosis.

Isolation of the Human Gax cDNA

The nucleotide sequence SEQ. ID. No. 3 of the human Gax gene coding sequence is shown in FIG. 3. Approximately 1×10^6 plaques from a human genomic library in λ FixII available from Stratagene were screened by conventional methods with a random primed EcoRI/BstXI fragment encompassing nucleotides 485-1151 of the rat Gax cDNA. Two clones contained the second exon of human Gax gene, having 182 base pairs. Using this coding information, the rest of the coding region was cloned by polymerase chain reaction methods.

Reverse transcriptase and polymerase chain reaction techniques were used to clone the 3' end of the human cDNA. The template was whole human RNA isolated from human internal mammary artery isolated by TRI reagent from Molecular Research Center, Inc. The following reagent concentrations were used in the reverse transcriptase reaction: 1 μ g of total internal mammary artery RNA; 50 mM Tris-HCl pH 8.5; 30 mM KCl; 8 mM MgCl₂; 1 mM DTT; 20 units RNasin from Boehringer Mannheim; 1 mM each of dATP, dTTP, dGTP, and dCTP; 0.5 μ g random hexamers from Boehringer Mannheim; and 40 u of AMV reverse transcriptase from Boehringer Mannheim, in a total volume of 20 μ L. This was incubated for 1 hour at 42° C., heat inactivated, and then stored at -80° C. before use. An initial amplification of 10% of the reverse transcriptase reaction was performed with just the sense oligonucleotide primer, known as "H2" and AmpliWax™ PCR Gem 100 beads Perkin Elmer in a "hot start" procedure according to the directions of the manufacturer. The following reagent concentrations were used: 50 mM KCl; 10 mM Tris-HCl at pH 8.3; 1.5 mM MgCl₂; 1 mg/mL gelatin; 0.2 mM each of dATP, dTTP, dGTP, and dCTP; 0.1 μ M primer(s); and 2.5 units of Taq polymerase from Boehringer Mannheim or Perkin Elmer in a volume of 100 μ L (these conditions were used thereafter unless noted). The cycling protocol was as follows: 94° C. for two minutes, then 30 cycles of 94° C. for 30 seconds, 45° C. for 1 minute, and 72° C. for 1 minute. A second amplification was then performed on 10% of the primary reaction products using the H2 primer and a degenerate antisense oligonucleotide primer known as "P2B" against the carboxy terminal peptide. The cycling parameters were: 94° C. for two minutes followed by 30 cycles of 94° C. for 30 seconds, 40° C. for 30 seconds, 50° C. for 1 minute and 72° C. for 1 minute. A product was observed of the correct size and following purification by Glass Fog from Bio101, on 2% Biogel agarose from Bio101 was blunt sub-cloned into EcoRV digested BluescriptII SK+ vectors

from Stratagene and sequenced to high resolution by Sequenase 2.0 from universal primers from United States Biochemical. Five individual clones were sequenced to eliminate any spurious Taq polymerase errors.

The 5' end of the human coding region was amplified using an anchored polymerase chain reaction kit, available under the tradename "5'-Amplifinder RACE" from Clonetech according to the manufacturer's instructions. This method uses single stranded RNA ligase to ligate an anchor oligonucleotide onto the 3' end of appropriately primed first strand cDNA. Templates used were either human heart polyA+ RNA obtained from Clonetech or polyA+ RNA isolated from primary cultures of human vascular smooth muscle cells obtained from Clonetics. The polyA+ RNA from cultured vascular smooth muscle cells was purified with RNAzol B from Bioteck using batch chromatography on Oligo-dT latex beads from Qiagen. Both templates yielded amplified cDNAs and specific subclones were chosen solely by size. First strand RNA templates were prepared by either specific priming or priming with random hexamers from Boehringer Mannheim. In general, the specific primed templates yielded longer clones but could not be used for multiple step wise amplification of the rest of the coding region.

Amplification from anchored templates using the sense anchor primer and appropriate antisense specific primers was accomplished using ampliWax beads from Perkin Elmer and "hot start" polymerase chain reaction using the same reaction conditions as above, but with 0.2 μ M primers in a total volume of 50 μ L. The cycling protocol was as follows: 94° C. for 2 minutes then 30 cycles of 94° C. 45 seconds, 60° C. 45 second, and 72° C. for 1.5 minutes, followed by a final extension of 72° C. for 10 minutes. Following a primary amplification, aliquots (10-20%) of the reactions were run out on 2% Biogel agarose from Bio101 and size selected. After purification by glass fog from Bio101, 1-10% of the elutes were reamplified (2^o), usually with a nested primer. Products were observed at this point and purified by glass fog as before and sequenced directly using a thermal cycling kit from New England Biolabs. Once the products were confirmed they were sub-cloned as described above. Between 5 to 8 individual clones from each of three sequential amplifications were sequenced to eliminate spurious Taq polymerase errors and appropriate clones chosen for the finished molecule. A summary of the primer pairs sense/antisense used to amplify the complete coding region:

position	Clone #	Source of Template	1°	2°	5'-3'
50	6	dN6 primed IMA whole RNA	H2	H2/P2B	699-941
	23	H2R primed Heart polyA + RNA	AP/H2R	AP/H3	231-698
	117	dN6 primed VSMC poly A + RNA	AP/H6	AP/H6	119-230
55	131	dN6 primed VSMC poly A + RNA	AP/H6	AP/H7	1-118

Clones were pieced together 3'-5' as follows: fragments 6 and 23 share engineered BglII sites; fragments 23 and 117 share a native SfaNI site; fragment 117 has a native NcoI site which is compatible with an engineered BspHI site in fragment 131. Both engineered sites have a single base change in the wobble base of leucine codons, as noted on the final sequence as shown in FIG. 3. Once assembled the molecule was excised by digestion with EcoRI and HindIII. The map in FIG. 4 shows the molecule and its orientation. The DNA molecule was deposited with the American Type

Culture Collection, 12301 Parklawn Drive, Rockville, Md. 20852, on Nov. 24, 1997, and was assigned Accession Number ATCC 209497.

mRNA was extracted. The total RNA from rat cultured cells was prepared by the guanidine thiocyanate method according to Chomczynski, P., and N. Sacchi, (1987) "Single-step

TABLE 1

Primers Used to Amplify Human Gax gene

Primer	Sequence 5'-3'
P2B SEQ. Id. No. 6	TCA,IA(G/A),(G/A)TG,IGC,(G/A)TG,(T/C)TC
H2 SEQ. Id. No. 7	GCGCGC(AGATCT)CAC,TGA,AAG,ACA,GGT,AAA
H2R SEQ. Id. No. 8	TT,TAC,CTG,TCT,ITC,AGT,GAG
H3 SEQ. Id. No. 9	GCGCGC(AGATCT)AG,ATT,CAC,TGC,TAT,CTC,GTG
H6 SEQ. Id. No. 10	GCGCGTGCCCCCGCTGATC,CTG,GCT,GGC,AAA,CAT,GT
H7 SEQ. Id. No. 11	GCGCGC(TCTTGA)AGG,GCG,AGA,GAG,GAT,TGG,GA
AP SEQ. Id. No. 12	CTGGTTGGGCCACCTCTGAAGGTTCCAGAACATCGATAG
Anchor SEQ. Id. No. 13	GGAGACTTCCAAGGTCTAGCTATCA(CTTAAG)CAC

Engineered enzyme sites are bracketed.

The Gax gene maps to a novel locus on Chromosome 7 in the human genome

To determine the map location of Gax in the human genome, a 16.5 kilobase pair fragment of the human genomic Gax gene in λ Fix II from Stratagene was purified with a Qiagen purification column according to the directions of the manufacturer, and it was labeled with biotin 11-dUTP by nick translation. Metaphase spreads of normal human lymphocytes were prepared according to the methods of Fan, Y., *Proc. Natl. Acad. Sci. (USA)* Vol. 87, pp. 6223-6227 (1990). Fluorescence *in situ* hybridization and immunofluorescence detection were performed according to the methods of Pinkel, D., et. al., *Proc. Natl. Acad. Sci. (USA)* Vol. 83, pp. 2934-2938 (1986) and Testa, J. R., et al. *Cytogenet. Cell. Genet.* Vol. 60, pp. 247-249 (1992). Chromosome preparations were stained with diamidino-2-phenylindole and propidium iodide according to Fan, Y. S., et. al., *Proc. Natl. Acad. Sci. (USA)* Vol. 87, pp. 6223-6227 (1990).

Forty metaphase spreads were examined with a Zeiss Axiophot fluorescence microscope, and fluorescent signals were detected on the short arm of chromosome 7 in 34 of these spreads. All signals were located at p15- \rightarrow p22, with approximately 70% of the signals at 7p21. Based on these data, Gax is the only homeoprotein known to map to this locus.

Gax gene expression is down-regulated in cultured vascular smooth muscle cells upon mitogen stimulation

It has been found that the Gax gene is expressed in quiescent vascular smooth muscle cells. Since platelet derived growth factor hereinafter also referred to as "PDGF" and other growth factors regulate vascular smooth muscle proliferation and differentiation, differences in Gax gene expression in response to PDGF and other mitogens such as fetal calf serum were examined in cultured vascular myocytes.

Cultures of rat smooth muscle cells were obtained from the media of aortas isolated from adult male Sprague-Dawley rats. Cells were seeded onto dishes in medium containing a 1:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 and supplemented with 10% newborn calf serum. Once established, the cells were maintained at 37° C. in a humidified atmosphere of 5% carbon dioxide, and subcultured within three days after reaching confluence. Vascular smooth muscle cells were labeled with monoclonal antibodies to smooth muscle α -actin from Sigma Chemical Co. to verify identity.

The cultured cells were exposed to various mitogens as discussed below. The cells were then harvested and the total

Method of RNA Isolation by Acid Guanidinium Thiocyanate-phenol-chloroform Extraction" *Anal. Biochem.* Vol. 162, pp. 156-159, fractionated on 1.2% agarose gels

containing formaldehyde, and blotted onto nylon membranes. The RNA from cultured cells was separated on 25 30-cm gels for transcript size determination and on 10-cm gels for other studies. Hybridizations were carried out at 65° C. in buffer containing 0.5M sodium phosphate at pH 7.0, 7% sodium dodecyl sulfate, 1 mM EDTA, and 1% bovine serum albumin, using a cDNA probe labeled by random

30 priming consisting of a truncated Gax cDNA lacking the 5' end and the CAX repeat, where the X may be cytosine or guanine. Probes for Hox-1.3 and Hox-1.4 consisted of the cDNAs isolated from the rat aorta library, and the probe for Hox-1.11 consisted of the DraI-EcoRI fragment of its cDNA. The blots were washed with a final stringency of 0.1

35 to 0.2 \times SSC-0.1% sodium dodecylsulfate at 65° C. After the probeings with the homeobox probes were complete, the blots were rehybridized with a probe to rat glyceraldehyde

40 3-phosphate dehydrogenase hereinafter also referred to as "GAPDH," to demonstrate message integrity. Gax mRNA and GAPDH mRNA were quantified with a Molecular Dynamics model 400S PhosphorImager to integrate band intensities, or by scanning densitometry of autoradiograms.

In all quantitative comparisons of Gax mRNA levels 45 between experimental groups, Gax mRNA levels were normalized to the corresponding GAPDH level determined on the same blot, to account for differences in RNA loading.

Time Course of GAX Down-regulation in Cultured Vascular Smooth Muscle Cells

Rat vascular smooth muscle cells, grown to a greater than 50 about 90% confluence, were placed in low-serum medium containing 0.5% calf serum for 3 days, to induce quiescence.

At this time, the medium was removed from the cells and replaced with fresh medium containing either 10% fetal calf serum or 10 ng/ml platelet derived growth factor from human platelets. The cells were then incubated for the

various times in the presence of either the fetal calf serum or the PDGF. As a control, quiescent cells were incubated with 55 fresh serum-free medium alone. The cells exposed to PDGF

60 were harvested at 0.25, 0.5, 1, 2, and 4 hours, and the cellular RNA isolated. The cells exposed to human fetal calf serum were harvested at 4, 24, and 48 hours. The Gax and the Hox

mRNA levels were determined by Northern blot analysis. Typical results are shown in FIGS. 5A and 5B.

65 A rapid down-regulation, that is a reduction in the amount of Gax mRNA, occurred in the vascular smooth muscle cells when they were stimulated with either fetal calf serum or

PDGF as shown in FIGS. 5A and 5B. The down-regulation ranged from 5- to nearly 20-fold, depending on the mitogen used and the experiment. The down-regulation typically occurred within 2 hours after stimulation with fetal calf serum or PDGF, and was maximal at 4 hours. Gax mRNA transcript levels began to recover significantly by approximately 24 hours and approached baseline between 24 and 48 hours after stimulation. The rate of recovery varied with the magnitude of the initial down-regulation and the individual cell culture preparations. While PDGF isolated from human platelets caused a rapid down-regulation of Gax, it had little or no effect on Hox-1.3 mRNA levels. Neither fetal calf serum nor any of the three isoforms of PDGF showed any effect on the transcript levels of Hox-1.3, Hox-1.4, or Hox-1.11, homeobox genes which were also isolated from the vascular smooth muscle library.

Magnitude of Gax Down-regulation Correlates with Potency of Mitogen

PDGF is a homodimer or heterodimer made of various combination of two chains, A and B. Thus, there are three isoforms of PDGF; PDGF-AA; PDGF-AB; and PDGF-BB; and they have differing potencies for stimulating DNA synthesis in rat vascular smooth muscle cells. The PDGF-AA, PDGF-AB and PDGF-BB were compared for their effect on Gax expression. Quiescent rat vascular smooth muscle cell received 10 ng/ml of either PDGF-AA, PDGF-AB, PDGF-BB, or 10% fetal calf serum. After 0, 1, 2, 4 and 8 hours the cells were harvested and the Gax mRNA level determined. The results are shown in FIG. 6.

As shown in FIG. 6, PDGF-AA did not down-regulate Gax gene expression in vascular smooth muscle cells, whereas the PDGF-AB and PDGF-BB isoforms, and the fetal calf serum reduced Gax gene expression approximately 10-fold by 4 hours. The greatest down-regulation occurred with the fetal calf serum followed by that with PDGF-BB and PDGF-AB.

To determine whether the extent of Gax gene down-regulation correlated with the potency of the mitogen used to stimulate the vascular smooth muscle cells, the ability of the three PDGF isoforms and fetal calf serum to stimulate DNA synthesis was measured by 3 H-thymidine uptake. Quiescent vascular smooth muscle cells were stimulated with one of the three PDGF isoforms, at 10 mg/ml, or 10% fetal calf serum. Then 5 μ Ci/ml 3 H-thymidine was added to the cultures for 1 hour at various time points as shown in FIG. 7. The cells were harvested and the 3 H-thymidine uptake was measured. The results are shown in FIG. 7.

The PDGF-AA at 10 ng/ml, which was ineffective in causing Gax gene down-regulation, only weakly stimulated DNA synthesis as shown in FIG. 7. PDGF-AB and PDGF-BB both stimulated cell proliferation as measured by 3 H-thymidine uptake at 15 hours. However, the fetal calf serum which was most effective at down regulating Gax gene expression, was also the most effective mitogen, that is it demonstrated the greatest 3 H-thymidine uptake.

Down-regulation of the Gax gene is Dependent on the Dose of the Mitogen

Dose-response experiments were conducted by stimulating quiescent vascular smooth muscle cells with either PDGF-AB, PDGF-BB or fetal calf serum at varying doses as shown in FIGS. 8 and 9. The effects on Gax mRNA levels were measured at 4 hours after mitogen stimulation. The results are shown in FIGS. 8 and 9.

As shown in FIG. 8, the dose response curves reveal that the 50% effective dose for Gax gene down-regulation 4 hours after PDGF-AB stimulation is between 4 and 8 ng/ml. The 50% effective dose for Gax gene down regulation 4

hours after PDGF-BB stimulation is between 2 and 5 ng/ml. The 50% effective dose for Gax down regulation 4 hours after fetal calf serum is approximately 1%, as shown in FIG. 9. Furthermore, 10% fetal calf serum suppresses Gax mRNA levels nearly 20-fold at 4 hours, an effect larger than that of a maximal stimulatory dose of PDGF-BB (30 ng/ml), which has a 10-fold effect, or of PDGF-AB, which has a less than 8-fold effect, as shown in FIG. 6. Thus, the down-regulation of Gax gene induced by either fetal calf serum or the different isoforms of PDGF correlates well with their abilities to stimulate DNA synthesis as measured by 3 H-thymidine uptake.

The Gax gene down-regulation is sensitive to low levels of mitogen stimulation, which cause a significant decrease in Gax mRNA levels. As shown in FIG. 9, stimulation of quiescent rat vascular smooth muscle cells with 1% fetal calf serum caused a 40% decrease in Gax mRNA levels after 4 hours. However, such stimulation increased 3 H-thymidine uptake less than two-fold over that observed in quiescent vascular smooth muscle cells (data not shown). Treatment with PDGF-BB at doses as low as 2 ng/ml, also caused a detectable decrease in the Gax mRNA level.

Gax Expression is Up-regulated or Induced when Synchronously Growing Cells Are Deprived of Serum

Sparingly plated vascular smooth muscle cells were grown in a medium containing 20% fetal calf serum, and then placed into serum free medium. The RNA was harvested at various times from 0 to 25 hours. The total mRNA was extracted and subjected to Northern Blot Analysis, then the mRNA transcript of Gax was quantified.

As shown in FIG. 10, the expression of the Gax gene was induced fivefold in vascular smooth muscle cells within 24 hours after the rapidly growing cells were placed in the serum-free medium. Thus, expression of Gax gene is regulated by the growth state of the cell, and its down-regulation is a prominent feature of the G_0/G_1 transition in these cells.

Gax Protein Inhibits Mitogen-Induced S Phase Entry in Vascular Smooth Muscle Cells

Production of Recombinant Proteins

To determine whether Gax gene exerts a negative control on cell growth in vascular smooth muscle cells, Gax gene was expressed as a glutathione S-transferase (hereinafter also referred to as "GST") fusion protein in bacteria and microinjected it into quiescent vascular smooth muscle cells. To determine the effect of the Gax protein on serum-induced cell proliferation, the effect of GST-Gax protein was compared to the effect of known protein regulators of cell growth.

To produce the Gax protein evaluated herein, the cDNA coding regions for Gax was fused in frame to the pGEX-2T expression vector obtained from Pharmacia Biotechnology, and then expressed in *E. coli*. Specifically, GST-Gax was produced according to the following procedure: the coding region of Gax cDNA spanning from nucleotides 200-1108 was amplified by polymerase chain reaction methods using the following primers:

5'GCGCGCGTCGACGAACACCCCTCTTGCG 3' SEQ. Id. No. 14 and

5'GCGCGCAAGCTTCATAAGTGTGCGTGCTC 3' SEQ. Id. No. 15

The resulting DNA was digested with Sall and HindIII restriction enzymes and cloned into Sall and HindIII sites in the polylinker of pGEM3-IT in vitro transcription translation vector described in Patel R. C. and Sen G. C. (1992) "Identification of the Double-stranded RNA-binding

Domain in the Human Interferon-inducible Protein Kinase," *J. Biol. Chem.* Vol. 267; pp. 7671-7676. The BamHI to Nael fragment of pGEM3-IT containing the Gax coding region was then sub-cloned into the same sites of pGEX-2T. The pGEX-2T vector with the YY1 cDNA, used to produce GST-YY1, was from Thomas Shenk at Princeton University.

The resultant glutathione S-transferase fusion proteins were purified by affinity chromatography on glutathione-agarose beads. *E. coli* XL1-blue cells were then transformed with the appropriate plasmid and were grown to a density of 0.6-0.8 A₅₀₀ and induced with 0.5 mM isopropyl-B-D-thiogalactopyranoside for 2 hours. The cells were harvested and lysed by ultrasonic vibration in phosphate buffered saline containing 1% triton x-100, 1 mM PMSF and 5 µg/ml aprotinin. The lysate was centrifuged at 15,000×g and the supernatant was collected. The supernatant was bound to the glutathione sepharose from Pharmacia (0.5 ml of resin per 100 ml of bacterial culture) for 2 hours on a rotator at 25 rpm. The slurry was pelleted by centrifugation at 1000×g for 2 minutes, then washed twice with complete lysis buffer then washed twice with lysis buffer lacking triton x-100. The bound protein was eluted for 30 minutes with phosphate buffered saline containing 10 mM reduced glutathione, from Sigma Chemical Company, 40 mM DTT and 150 mM NaCl. Purity of the GST-Gax protein was greater than 90% as determined by SDS-PAGE gels stained with Coomassie blue.

To produce recombinant MHox, its cDNA was fused in frame to the pQE-9 *E. coli* expression vector obtained from Qiagen, Inc., Chatsworth, Calif., then expressed in bacteria, and purified by adsorption to a nickel column.

For microinjection, proteins were concentrated in a buffer containing of 20 mM Tris, 40 mM KC1, 0.1 mM EDTA, 1 mM β-mercaptoethanol, and 2% glycerol using Centri-con-30 from Amicon microconcentrators. Concentrated proteins were stored in this buffer in aliquots at -80° C.

Microinjection and Cell Culture Methods

Microinjections were performed using a semiautomatic microinjection system from Eppendorf Inc. in conjunction with a Nikon Diaphot phase contrast microscope. According to Peperkole, R., et al. (1988) *Proc. Natl. Acad. Sci. USA* Vol. 85, pp. 6758-6762, The injection pressure was set at 70-200 hPa and the injection time was 0.3 to 0.6 seconds.

After injection, cells were stimulated 24 hours with medium containing 10% fetal calf serum, and the incorporation of 5'-bromo-2'-deoxyuridine, hereinafter also referred to as "BrdU" was measured with a cell proliferation kit according to the directions of its manufacturer, Amersham. When fetal calf serum-stimulated BrdU labeling was determined, BrdU was included for 24 hours with the medium used to stimulate the cells. Where the ability of microinjected proteins to stimulate growth in serum-poor medium was measured, cells were incubated 24 hours in the same low serum medium used to induce quiescence, but supplemented with BrdU. After labeling, the cells were fixed with acid-ethanol, and the percentage of nuclei positive for BrdU uptake was determined for protein-injected and buffer-injected cells. The percent of cell growth inhibition was calculated according to the following formula:

$$\% \text{ Inhibition} = \frac{\frac{CL}{CT} - \frac{IL}{IT}}{\frac{CL}{CT}} \times 100$$

where IL represents the number of injected labeling positive for BrdU; IT, the total number of injected cells; CL the number of control-injected cells labeling with BrdU; CT, the

total number of control-injected cells counted. With this equation, inhibition of mitogen-induced entry into S phase is represented by a positive number and stimulation of cell growth is represented by a negative number.

Evaluation of Gax Protein

To determine if the Gax protein inhibits the entry of mitogen stimulated vascular smooth muscle cells into S-phase, the effect of the Gax protein was compared to proteins known to effect cell proliferation, and to control proteins. Such comparison proteins include a neutralizing antibody against ras, "Y13-259," which is highly effective in blocking S phase entry when microinjected into NIH3T3 cells; the transcription factor MHox, a homeodomain protein unlikely to have an inhibitory effect on cell proliferation; and YY1, a zinc finger transcription factor unlikely to have a negative effect on cell growth.

Quiescent rat vascular smooth muscle cells were microinjected with either 0.6 mg/ml GST-Gax-protein; 1.6 mg/ml MHox; 1.2 mg/ml YY1; 8 mg/ml Y13-259; 2 mg/ml GST alone; or 8 mg/ml mouse anti-human IgG. The cells were then stimulated for 24 hours with 10% fetal calf serum in medium containing BrdU. After 24 hours, the fraction of nuclei labeling with BrdU was determined and percentage inhibition of S-phase entry calculated. The results are summarized in Table 2.

TABLE 2

Effect of Microinjected Proteins on the Serum-induced Proliferation of Vascular Smooth Muscle Cells			
Treatment	Number of Experiments	Total Number of Cells Examined	Mean % Inhibition of FCS-stimulated Growth ± Standard Error
Antibody Y13-259	2	328	60.8 ± 3.9
Mouse anti-human IgG	3	330	-3.4 ± 4.5
GST-Gax	15	2943	42.7 ± 3.3
MHox	2	236	-5.3 ± 9.3
GST-YY1	5	306	0.0 ± 12.2
GST	7	1144	-2.6 ± 2.1

40 FCS — fetal calf serum
BrdU labeling of quiescent vascular smooth muscle cells was 10.1 ± 1.2% (N = 12, total number of cells counted = 2659); for uninjected FCS-stimulated vascular smooth muscle cells, 54.8 ± 2.4% (N = 27, total number of cells counted = 4282); and for sham-injected FCS-stimulated cells, 49.6 ± 2.5% (N = 27, total number of cells injected = 3401).

45 As shown in Table 2, the GST-Gax protein inhibited vascular smooth muscle cell entry into S-phase by 42.7%. The GST Gax protein effect on mitogen-stimulated entry into S phase is specific. The other injected proteins GST, YY1, MHox and the mouse anti-human IgG failed to inhibit vascular smooth muscle cell growth. In comparison to the GST-Gax protein, the antibody Y13-259, as anticipated, significantly decreased mitogen-induced cell proliferation. Vascular smooth muscle cells microinjected with Y13259 demonstrated a 61±4% decrease in cell entry into S-phase. Gax Protein Inhibits Vascular Smooth Muscle Cell Proliferation in a Dose-Dependent Manner.

To determine the concentration of microinjected GST-Gax required to inhibit vascular smooth muscle cell growth, 50 solutions containing different concentrations of GST-Gax protein were microinjected into quiescent vascular smooth muscle cell and the effects on mitogen-stimulated entry into S phase examined. Specifically, vascular smooth muscle cells were rendered quiescent by incubation in medium containing 0.5% calf serum for three days. The cells were microinjected with varying concentrations of GST-Gax, and stimulated with 10% fetal calf serum, and labeled with

BrdU. After 24 hours, the percentage inhibition of cell proliferation was determined. Each data point represents the mean \pm standard error of 3-5 experiments in which 100-200 cells per experimental group were injected.

As shown in FIG. 11, the cellular growth inhibition by the GST-Gax protein is dose dependent. Little or no growth inhibition was observed when 0.2 mg/ml GST-Gax protein was injected. The maximal growth inhibition was obtained with approximately 0.5 mg/ml of the GST-Gax protein.

Gax Inhibits Proliferation of Several Cell Types

To determine whether the GST-Gax protein inhibits growth in other cell types, the GST-Gax protein was microinjected into quiescent SV40-transformed vascular smooth muscle cells, BALBc3T3 cells, NIH3T3 cells, human vascular smooth muscle cells, and human fibroblasts. The SV40 transformed cell line was derived from rat vascular smooth muscle cells transformed with the SV40 large T antigen. These cells, while immortalized, retain many differentiated characteristics of untransformed vascular smooth muscle cells. The cells were microinjected with either 0.6 mg/ml GST-Gax protein or 2 mg/ml GST were then stimulated with 10% fetal calf serum, and labeled for 24 hours with BrdU. The results are shown in Table 3.

An Oncogenic Ras Protein Can Reverse Growth Inhibition Caused by the Gax protein

To characterize the mechanism of the growth inhibition conferred by the GST-Gax protein, the effects of GST-Gax protein and the transforming oncoprotein, the ras mutant Ras(Leu-61) were compared by microinjecting these proteins into rat vascular smooth muscle cells. A solution containing both 0.5 mg/ml GST-Gax protein and 0.5 mg/ml Ras(Leu-61) was microinjected into quiescent vascular smooth muscle cells. For comparison, other vascular smooth muscle cells received either 0.5 mg/ml GST-Gax protein or 0.5 mg/ml Ras(Leu-61) or 0.5 mg/ml GST. The injected cells were then incubated for 24 hours with medium containing 10% fetal calf serum and BrdU. The results are shown in FIG. 12.

As shown in FIG. 12, when Ras(Leu-61) alone was injected, there was an increase in BrdU-labeling as compared to both control-injected cells. In cells injected with GST-Gax protein, growth was inhibited 39%. When the GST-Gax protein and Ras(Leu-61) were coinjected in the cells, the Ras(Leu-61) reversed the growth inhibitory effects of the GST-Gax protein, and the percentage of cells staining positive for BrdU in cells receiving both the Ras(Leu-61)

TABLE 3

EFFECT OF MICROINJECTED GST-GAX PROTEIN ON CELL PROLIFERATION IN DIFFERENT CELL TYPES

Cell type	GST-GAX protein	Number of Experiments	Number of Cells Examined	Mean & Range Inhibition of FCS-Stimulated Growth	Mitotic Index in Response to FCS
SV40-transformed VSMC	Yes	4	448	27.2 \pm 2.0	—
SV40-transformed VSMC	No			N/A	0.60 \pm 0.02
BALB/c 3T3 cells	Yes	4	464	30.5 \pm 10.9	—
BALB/c 3T3 cells	No			N/A	0.64 \pm 0.03
NIH3T3 cells	Yes	4	420	23.2 \pm 1.8	—
NIH3T3 cells	No			N/A	0.70 \pm 0.02
Human VSMC	Yes	3	506	46.6 \pm 8.1	—
Human VSMC	No			N/A	0.33 \pm 0.02
Human fibroblasts	Yes	3	336	44.5 \pm 2.1	—
Human fibroblasts	No			N/A	0.36 \pm 0.01

FCS — fetal calf serum

VSMC — vascular smooth muscle cells

SV40-transformed vascular smooth muscle cell proliferation was inhibited by GST-Gax protein, as shown in Table 3. The GST-Gax protein also inhibited the proliferation of fibroblast cell lines NIH3T3 and BALB/c 3T3. GST-Gax protein also inhibited the proliferation of human cells, specifically human vascular smooth muscle cells and human foreskin fibroblasts. These results indicate that Gax action is not cell type-specific, although there are differences in the extent inhibition among the different cell types. Among the human cells, the GST-Gax protein exhibits maximal inhibition in vascular smooth muscle cells, the cell type in which the Gax gene is normally expressed. Similarly among the rat cells, the GST-Gax protein exhibits maximal inhibition in vascular smooth muscle cells, the cell type in which the Gax gene is normally expressed.

and GST-Gax protein were nearly identical to that observed in cells receiving just the Ras(Leu-61). Thus, the Ras oncoprotein completely reversed the effect of the GST-Gax protein establishing that the presence of GST-Gax protein is not toxic to cells.

The Gax Protein Inhibits Cell Growth when Microinjected Before the G1 to S Boundary

To determine the point in the cell cycle when the Gax gene exerts its growth inhibitory effects, the time of S phase onset was determined in rat vascular smooth muscle cells. The vascular smooth muscle cells were stimulated with 10% fetal calf serum and pulse labeled with 10 mCi/ml ³H-thymidine for one hour at different times after stimulation. Separate cultures of the cells were microinjected with GST-Gax protein at various times after receiving 10% fetal calf serum and labeled with BrdU between 10 and 24 hours

after receiving the fetal calf serum. Percent inhibition of S-phase entry was determined at each time point. The results are shown in FIG. 13.

As shown in FIG. 13, S phase onset, indicated by the uptake of ³H-thymidine, occurred at approximately 16-18 hours after mitogen stimulation. GST-Gax protein significantly inhibited vascular smooth muscle cell entry into the S phase when microinjected at any time from stimulation up until approximately 12 hours. However, GST-Gax protein was ineffective when injected at 15 hours. Thus it appears that the Gax gene inhibits a critical step in cell cycle progression prior to the G₁/S boundary; perhaps before the restriction point in G₁ where eukaryotic cells are irreversibly committed to entering the S phase.

Gax Gene Expression is Rapidly Down Regulated in Vivo Upon Acute Blood Vessel Injury

The Gax gene expression in normal blood vessels and in injured blood vessels was compared to determine whether Gax gene down-regulation occurs in response to injury-induced smooth muscle cell proliferation in vivo. Adult male Sprague-Dawley rats were subject to acute vessel injury by balloon de-endothelialization in the carotid arteries according to the methods of Majesky, M. W., et al. *J. Cell. Biol.* (1990) Vol. 111, pp. 2149-2158. The expression levels of Gax, that is, the mRNA levels, were assessed relative to that of glyceraldehyde 3-phosphate dehydrogenase (hereinafter also referred to as "G3") by a quantitative polymerase chain reaction. At various times following balloon de-endothelialization the rats were sacrificed and the total RNA was isolated from the vascular smooth muscle tissues using the TRI reagent from Molecular Research Center, Inc. The cDNA was synthesized from the extracted RNA with MMLV reverse transcriptase from Bethesda Research Labs. Aliquots of the cDNA pools were subjected to polymerase chain reaction amplification with AmpliTaq DNA polymerase from Perkin-Elmer in the presence of a32P-dCTP with the following cycle conditions: 94° C. for 20 seconds, 55° C. for 20 seconds, and 72° C. for 20 seconds. The final cycle had an elongation step at 72° C. for 5 minutes. The primers for the rat Gax amplification were: 5'-CCCGCGCGGCTTTACATTAGGAGT-3' SEQ. Id. No. 16 and 5'-GCTGGAAACATGCCCTCCTCAITG-3' SEQ. Id. No. 17. The primers for the rat G3 gene were 5'-TGATGGCATGGACTGTGGTCATGA-3' SEQ. Id. No. 18 and 5'-TGATGGCATGGACTGTGGTCATGA-3' SEQ. Id. No. 19. The Gax cDNA was amplified for 30 cycles, and G3

was amplified for 25 cycles in the same reaction vessels. The amount of a radioactive label incorporated into the amplified cDNA and G3 fragments was determined by subjecting the fragments to electrophoresis on a 1% agarose gel, then excising the bands and liquid scintillation counting. Since the mRNA levels of glyceraldehyde 3-phosphate dehydrogenase remain relatively constant following this procedure (see J. M. Miano et al. 1990, *Am. J. Path.* 137, 761-765), the ratio of radiolabel incorporation into the Gax-derived amplified bands and the G3-derived amplified bands corrects for differences arising from the efficiency of RNA extraction from the different animals, and it provides a measure of Gax mRNA levels in the normal and injured vascular tissues. These ratios are plotted in FIG. 14.

As shown in FIG. 14, the Gax mRNA expression was down-regulated in response to acute vessel injury by as much as a factor of 20. This down-regulation was rapid and appeared complete by 2 hours, the first time-point following the de-endothelialization procedure. Collectively, these data corroborate the Gax gene down-regulation in cultures of vascular smooth muscle cells following growth factor stimulation. Further, these data show that Gax gene expression is an early marker of the cell cycle activity associated with the initiation of vascular restenosis, and they indicate that Gax has a regulatory role following blood vessel injury.

The present invention includes: the DNA sequences encoding a protein, or portion thereof, which inhibits vascular smooth muscle cell proliferation; the messenger RNA transcript of such DNA sequence; and an isolated protein which inhibits vascular smooth muscle cell growth.

For example, the DNA sequences include: DNA molecules which, but for the degeneracy of the genetic code would hybridize to DNA encoding the Gax protein, thus the degenerate DNA which encodes the Gax protein; DNA strands complementary to DNA sequences encoding the Gax protein or portions thereof including DNA in FIGS. 1 and 3 or portions thereof; heterologous DNA having substantial sequence homology to the DNA encoding the Gax protein, including the DNA sequences in FIGS. 1 and 3 or portions thereof.

The isolated protein includes, for example, portions of the Gax protein; the Gax protein of animals other than rat and human; and proteins or portions thereof having substantially the same amino acid sequence as shown in FIGS. 1 and 3 or portions thereof.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i i i) NUMBER OF SEQUENCES: 19

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

SEARCHED
INDEXED
SEARCHED
INDEXED
SEARCHED
INDEXED
SEARCHED
INDEXED

-continued

(i x) FEATURE

(A) NAME/KEY: CDS
(B) LOCATION: 197..1108

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTC	AAAGT	GTT	TAT	ACGT	GCA	GGAGACT	GGC	CGCTCGG	CTC	AGGACT	GGGA	TTAGCGGG	C	60		
CTG	CTCAA	AC	CCG	CGC	GGCT	TTTACATT	AG	GAGTGACT	GG	GGGAGAGT	CC	TAGGATT	TCT	120		
AGT	AAAAAGT	GACAGCC	CTT	GGTGGACT	TTT	GGGACCT	TCG	TGAAGTC	CTTC	TGCTT	GGAA	G	180			
CTGAGACT	TG	CATGCC	ATG	GAA	CAC	CCC	CTC	TTT	GGC	TGC	CTG	CGC	AGC	229		
			Met	Glu	His	Pro	Leu	Phe	Gly	Cys	Leu	Arg	Ser			
			1	5							10					
CCC	CAC	GCC	ACA	GCG	CAA	GGC	TTG	CAC	CCC	TTC	TCG	CAG	TCT	TCT	CTG	277
Pro	His	Ala	Thr	Ala	Gln	Gly	Leu	His	Pro	Phe	Ser	Gln	Ser	Ser	Leu	
			15				20					25				
GCC	CTC	CAT	GGA	AGA	TCT	GAC	CAC	ATG	TCC	TAC	CCC	GAA	CTC	TCC	ACA	325
Ala	Leu	His	Gly	Arg	Ser	Asp	His	Met	Ser	Tyr	Pro	Glu	Leu	Ser	Thr	
			30				35					40				
TCT	TCC	TCG	TCT	TGC	ATA	ATC	GGC	GG	TAC	CCC	AAT	GAG	GAG	GGC	ATG	373
Ser	Ser	Ser	Ser	Cys	Ile	Ile	Ala	Gly	Tyr	Pro	Asn	Gln	Gln	Gly	Met	
			45				50					55				
TTT	GCC	AGC	CAG	CAT	CAC	AGG	GGG	CAC	CAC	CAC	CAC	CAC	CAC	CAC	CAC	421
Phe	Ala	Ser	Gln	His	His	Arg	Gly	His	His	His	His	His	His	His	His	
			60			65			70			75				
CAT	CAC	CAC	CAC	CAG	CAG	CAG	CAG	CAC	GCT	CTG	CAA	AGC	AAC	TGG	469	
His	His	His	His	Gln	Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	Ser	Asn	Trp	
			80			85			90							
CAC	CTC	CCG	CAG	ATG	TCC	TCC	CCG	CCA	AGC	GCG	GCC	CGG	CAC	AGC	CTT	517
His	Leu	Pro	Gln	Met	Ser	Ser	Pro	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	
			95			100						105				
TGC	CTG	CAG	CCT	GAT	TCC	GG	GGG	CCC	CCG	GAG	CTG	GGG	AGC	AGC	CCT	565
Cys	Leu	Gln	Pro	Asp	Ser	Gly	Gly	Pro	Pro	Gln	Leu	Gly	Ser	Ser	Pro	
			110			115			120							
CCG	GTC	CTG	TGC	TCC	AAC	TCT	TCT	AGC	CTG	GGC	TCC	AGC	ACC	CCG	ACC	613
Pro	Val	Leu	Cys	Ser	Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	
			125			130			135							
GGA	GCC	GCG	TGC	GCA	CCA	AGG	GAT	TAT	GGC	CGT	CAA	GCG	CTG	TCA	CCC	661
Gly	Ala	Ala	Cys	Ala	Pro	Arg	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro	
			140			145			150			155				
GCA	GAA	GTG	GAG	AAG	AGA	AGT	GGC	AGC	AAA	AGA	AAA	AGC	GAC	AGT	TCA	709
Ala	Glu	Val	Glu	Lys	Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser	
			160			165			170							
GAT	TCC	CAG	GAA	GGA	AAT	TAC	AAG	TCA	GAA	GTG	AAC	AGC	AAA	CCT	AGG	757
Asp	Ser	Gln	Glu	Gly	Asn	Tyr	Lys	Ser	Gln	Val	Asn	Ser	Lys	Pro	Arg	
			175			180			185							
AGG	GAA	AGA	ACA	GCT	TTC	ACC	AAA	GAG	CAA	ATC	AGA	GAA	CTT	GAG	GCA	805
Arg	Glu	Arg	Thr	Ala	Phe	Tbr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala	
			190			195			200							
GAG	TTC	GCC	CAT	CAT	AAC	TAT	CTG	ACC	AGA	CTG	AGA	AGA	TAT	GAG	ATA	853
Gln	Phe	Ala	His	His	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Arg	Tyr	Gln	
			205			210			215							
GCG	GTG	AAC	CTA	GAC	CTC	ACT	GAA	AGA	CAG	GTG	AAA	GTG	TGG	TTC	CAG	901
Ala	Val	Asn	Leu	Asp	Leu	Thr	Gln	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln	
			220			225			230			235				
AAC	AGG	AGA	ATG	AAG	TGG	AAG	CGG	GTC	AAG	GGG	GG	CAA	CAA	GGA	GCT	949
Asn	Arg	Arg	Met	Lys	Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala	
			240			245			250			250				
GCA	GCC	CGA	GAA	AAG	GAA	CTG	GTG	AAT	GTG	AAA	AAG	GGA	ACA	CTT	CTT	997
Ala	Ala	Arg	Glu	Lys	Gln	Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	
			255			260			265			265				

5,856,121

21

22

-continued

CCA TCA GAG CTG TCA GGA ATT GGT GCA GCC ACC CTC CAG CAG ACA GGG	1045
Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly	
270 275 280	
GAC TCA CTA GCA AAT GAC GAC AGT CGC GAT AGT GAC CAC AGC TCT GAG	1093
Asp Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu	
285 290 295	
CAC GCA CAC TTA TGATACATAC AGAGACCAGC TCCGTTCTCA GGAAAGCACC	1145
His Ala His Leu	
300	
ATTTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCACTGTTG	1205
CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC	1265
ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAATT GGAGAAAGTG AACATATCTA	1325
AATATACTTG TTCCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTGG CTTGCACTGA	1385
AAATTAATT GCTACCAAGA GCAAACCTCGG TAAGACATT TGACTCAAGT TGTCTCCAGA	1445
GTGAAGATGT TATAGAAATG CTTGAACAT TCCAGTTGTA CCAGGTCATG TGTGTGACAC	1505
TGGCAGGTA TTTGCTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA	1565
AATAGTTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAACTG	1625
AAATTCTGTA TATATTACTC CTAAGTCATT TTCTGTCTT CACTAATTAG AGCAAATGCA	1685
TTCATATTAG CTGATGAAAA TAGGCTTCC CGTGGACAAA TGCAGCCAGC TTCTTGTATT	1745
TTTATACATT TTTTGTCAAG TCAGAGACAT CAGTATGTGC TTACTTGTGT TCAAGTAGAG	1805
GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG	1865
TTGCATTGAC TATCAACTGTC TGCAGATACA TTAGAGAACAA CACCTAGCCC CCCTCCAGCC	1925
TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA	1985
GTCTTGTGTG GCAGATGTCT GATTTGTAT CTTTAAACTG TTAATGGTAT GTGTCTGCTT	2045
CAGTTAACAG GGAAAAAGAT TTCTTCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA	2105
CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA	2165
AAATACATTA TTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTGTAAA	2225
AAAAAAAGTT AAATAAATG	2244

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala	
1 5 10 15	
Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg	
20 25 30	
Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys	
35 40 45	
Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His	
50 55 60	
His Arg Gly His Gln	
65 70 75 80	
Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met	
85 90 95	

-continued

Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Glu	Pro	Asp
100								105					110		
Ser	Gly	Gly	Pro	Pro	Gly	Leu	Gly	Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser
115								120					125		
Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala
130								135				140			
Pro	Arg	Asp	Tyr	Gly	Arg	Gly	Ala	Leu	Ser	Pro	Ala	Glu	Val	Glu	Lys
145								150				155			160
Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser	Asp	Ser	Gly	Gly	
165								170					175		
Asn	Tyr	Lys	Ser	Gly	Val	Asn	Ser	Lys	Pro	Arg	Arg	Gly	Arg	Thr	Ala
180								185					190		
Phe	Thr	Lys	Gly	Gly	Ile	Arg	Gly	Leu	Gly	Ala	Glu	Phe	Ala	His	His
195								200				205			
Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Gly	Ile	Ala	Val	Asn	Leu	Asp
210								215				220			
Leu	Thr	Gly	Arg	Gly	Val	Lys	Val	Trp	Phe	Gly	Asn	Arg	Arg	Met	Lys
225								230				235			240
Trp	Lys	Arg	Val	Lys	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Arg	Gly	Lys	
245								250				255			
Gly	Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	Pro	Ser	Gly	Leu	Ser
260								265				270			
Gly	Ile	Gly	Ala	Ala	Thr	Leu	Gly	Gly	Thr	Gly	Asp	Ser	Leu	Ala	Asn
275								280				285			
Asp	Asp	Ser	Arg	Asp	Ser	Asp	His	Ser	Ser	Gly	His	Ala	His	Leu	
290								295				300			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 33..941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCTTCTACC	TGGAAACCCGA	AACTTGCATG	CT	ATG	GAA	CAC	CCG	CTC	TTT	GGC			53		
											1	5			
TGC	CTG	CGC	AGC	CCT	CAC	GCC	GCG	CAA	GGC	TTG	CAC	CCG	TTC	TCC	101
											10	15	20		
CAA	TCC	TCT	GCC	CTC	CAT	GGA	AGA	TCT	GAC	CAT	ATG	TCT	TAC	CCC	149
											25	30	35		
GAG	CTC	TCT	ACT	TCT	TCC	TCA	TCT	TGC	ATA	ATC	GCG	GGA	TAC	CCC	197
											40	45	50	55	
GAA	GAG	GAC	ATG	TTT	GCC	AGC	CAG	CAT	CAC	AGG	GGG	CAC	CAC	CAC	245
											60	65	70		

-continued

CAC	CAC	CAC	CAT	CAC	CAC	CAT	CAG	CAG	CAG	CAG	CAC	CAG	GCT	CTG	CAA	293
His	Gln	Gln	Gln	Gln	His	Gln	Ala	Leu	Gln							
75							80						85			
ACC	AAC	TGG	CAC	CTC	CCG	CAG	ATG	TCT	TCC	CCA	CCG	AGT	GCG	GCT	CGG	341
Thr	Asn	Trp	His	Leu	Pro	Gln	Met	Ser	Ser	Pro	Pro	Pro	Ser	Ala	Ala	Arg
90							95						100			
CAT	AGC	CTC	TGC	CTC	CCG	CAG	GAC	TCT	GGA	GGG	CCC	CCA	GAG	TTG	GGG	389
His	Ser	Leu	Cys	Leu	Gln	Pro	Asp	Ser	Gly	Gly	Pro	Pro	Gly	Leu	Gly	
105							110						115			
AGC	AGC	CCG	CCC	GTC	CTG	TGC	TCC	AAC	TCT	TCC	AGC	TTG	GGC	TCC	AGC	437
Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser	Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	
120							125					130			135	
ACC	CCG	ACT	GGG	GCC	GCG	TGC	GCG	CCG	GGG	GAC	TAC	GGC	CGC	CAG	GCA	485
Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala	Pro	Gly	Asp	Tyr	Gly	Arg	Gln	Ala	
140							145						150			
CTG	TCA	CCT	GCG	GAG	GCG	GAG	AAG	CGA	AGC	GGC	GGC	AAG	AGG	AAA	AGC	533
Leu	Ser	Pro	Ala	Glu	Ala	Glu	Lys	Arg	Ser	Gly	Gly	Lys	Arg	Lys	Ser	
155							160						165			
GAC	AGC	TCA	GAC	TCC	CAG	GAA	GGA	AAT	TAC	AAG	TCA	GAA	GTC	AAC	AGC	581
Asp	Ser	Asp	Ser	Gln	Gln	Gly	Asn	Tyr	Lys	Ser	Gln	Val	Asn	Ser		
170							175						180			
AAA	CCC	AGG	AAA	GAA	AGG	ACA	GCA	TTT	ACC	AAA	GAG	CAA	ATC	AGA	GAA	629
Lys	Pro	Arg	Lys	Glu	Arg	Thr	Ala	Phe	Thr	Lys	Gln	Ile	Arg	Gln		
185							190						195			
CTT	GAA	GCA	GAA	TTT	GCC	CAT	CAT	AAT	TAT	CTC	ACC	AGA	CTG	AGG	CGA	677
Leu	Glu	Ala	Glu	Phe	Ala	His	His	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	
200							205					210			215	
TAC	GAG	ATA	GCA	GTG	AAT	CTG	GAT	CTC	ACT	GAA	AGA	CAG	GTA	AAA	GTC	725
Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp	Leu	Thr	Gly	Arg	Gln	Val	Lys	Val	
220							225						230			
TGG	TTC	CAA	AAC	AGG	CGG	ATG	AAG	TGG	AAG	AGG	GTA	AAG	GGT	GGA	CAG	773
Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys	Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	
235							240						245			
CAA	GGA	GCT	GCG	GCT	CGG	GAA	AAG	GAA	CTG	GTG	AAT	GTG	AAA	AAG	GGA	821
Gln	Gly	Ala	Ala	Ala	Arg	Glu	Lys	Glu	Leu	Val	Asn	Val	Lys	Lys	Gly	
250							255						260			
ACA	CTT	CTC	CCA	TCA	GAG	CTG	TCG	GGA	ATT	GGT	GCA	GCC	ACC	CTC	CAG	869
Thr	Leu	Leu	Pro	Ser	Glu	Leu	Ser	Gly	Ile	Gly	Ala	Ala	Thr	Leu	Gln	
265							270						275			
CAA	ACA	GGG	GAC	TCT	ATA	GCA	AAT	GAA	GAC	AGT	CAC	GAC	AGT	GAC	CAC	917
Gln	Thr	Gly	Asp	Ser	Ile	Ala	Asn	Glu	Asp	Ser	His	Asp	Ser	Asp	His	
280							285						290			295
AGC	TCA	GAG	CAC	GCC	CAC	CTC	TGA									941
Ser	Ser	Glu	His	Ala	His	Leu										
300																

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
 1 5 10 15

Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
 20 25 30

Ser Asp His Met Ser Tyr Pro Gln Leu Ser Thr Ser Ser Ser Cys
 35 40 45

-continued

Ile Ile Ala Gly Tyr Pro Asn Glu Glu Asp Met Phe Ala Ser Gln His
 50 55 60

His Arg Gly His Gln Gln
 65 70 75 80

Gln Gln His Gln Ala Leu Gln Thr Asn Trp His Leu Pro Gln Met Ser
 85 90 95

Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp Ser
 100 105 110

Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser Asn
 115 120 125

Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala Pro
 130 135 140

Gly Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Ala Glu Lys Arg
 145 150 155 160

Ser Gly Gly Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Gln Gly Asn
 165 170 175

Tyr Lys Ser Gln Val Asn Ser Lys Pro Arg Lys Gln Arg Thr Ala Phe
 180 185 190

Thr Lys Gln Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His Asn
 195 200 205

Tyr Leu Thr Arg Leu Arg Arg Tyr Gln Ile Ala Val Asn Leu Asp Leu
 210 215 220

Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys Trp
 225 230 235 240

Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys Glu
 245 250 255

Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Gln Leu Ser Gly
 260 265 270

Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Ile Ala Asn Glu
 275 280 285

Asp Ser His Asp Ser Asp His Ser Ser Glu His Ala His Leu
 290 295 300

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod_base=i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /mod_base=i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /mod_base=i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5,856,121

29

30

-continued

A A R A T W T G G T T Y C A R A A Y M G W M G W A T G A A

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: YES

(i x) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 4
(D) OTHER INFORMATION: /mod_base= i

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:6:

T C A W A R R T G W G C R T G Y T C

18

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:7:

G C G C G C A G A T C T C A C T G A A A G A C A G G T A A A

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: YES

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

T T T A C C T G T C T T T C A G T G A G

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: YES

5,856,121

31

32

-continued

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GC GCG CAG AT CTAG ATT CAC TGCT AT CT CG TA

32

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: YES

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGCGT GCCC CCTCTG AT GC TGGCTGGCAA ACATGT

36

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGCGCTCTT GAAGGGCGAG AGAGGATTGG GA

32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGTT CGGC CCACCTCTGA AGGT TCCAGA ATCGATAG

38

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGACTTCC AAGGTCTTAG CTATCACTTA AGCAC

35

(2) INFORMATION FOR SEQ ID NO:14:

-continued

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCGCGTCG ACGAACACCC CCTCTTTGGC

3 0

(2) INFORMATION FOR SEQ ID NO:15:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCGCAAGC TTTCATAAGT GTGCGTGCTC

3 0

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCGCGCGGC TTTTACATTA GGAGT

2 5

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(i i i) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGGCAAAC ATGCCCTCCT CATTG

2 5

(2) INFORMATION FOR SEQ ID NO:18:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear